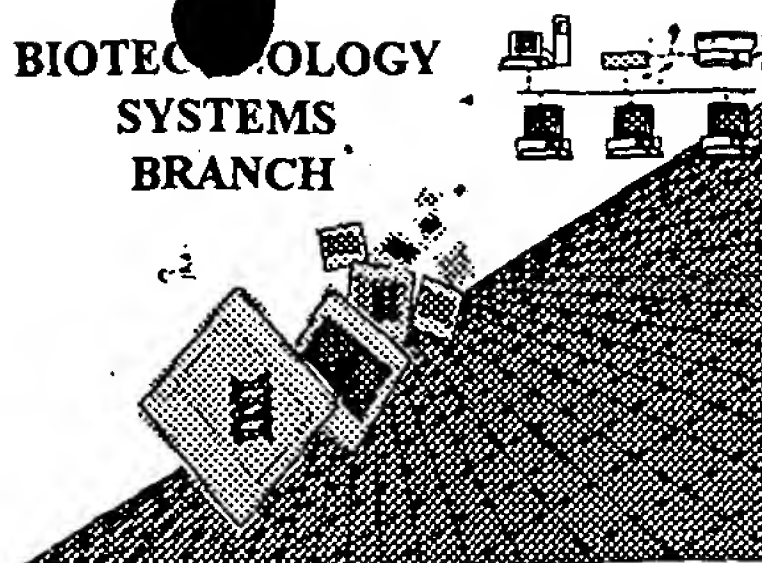


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/665,308A

Source: OIR

Date Processed by STIC: 7/31/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/665,308A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

#128P
9/27/01
OIPERAW SEQUENCE LISTING
PATENT APPLICATION: US/09/665,308ADATE: 07/31/2001
TIME: 14:45:58Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.rawDoes Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Cahoon, Rebecca E.
 4 Klein, Theodore M.
 5 Odell, Joan T.
 6 Orozco, Emil M. Jr.
 8 <120> TITLE OF INVENTION: PLANT CELL CYCLIN GENES
 10 <130> FILE REFERENCE: BB1149 US NA
 12 <140> CURRENT APPLICATION NUMBER: US/09/665,308A
 12 <141> CURRENT FILING DATE: 2000-09-19
 12 <150> PRIOR APPLICATION NUMBER: 60/078,735
 13 <151> PRIOR FILING DATE: 1998 March 20 1998-03-20 use this date format
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/06047
 16 <151> PRIOR FILING DATE: 1999 March 19 1999-03-19
 18 <160> NUMBER OF SEQ ID NOS: 32
 20 <170> SOFTWARE: MICROSOFT OFFICE 97

RRORED SEQUENCES

1053 <210> SEQ ID NO: 21
 1054 <211> LENGTH: 789
 1055 <212> TYPE: DNA
 1056 <213> ORGANISM: Triticum aestivum
 1058 <400> SEQUENCE: 21
 1059 cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat 60
 1060 ctccaccgct cgaccaaagt gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120
 1061 aaagtgatgg agcttttggt cttcagcacc ttgaaatgga ggatgcaagc tgttactgct 180
 1062 tgctcgttta ttgactactt cctttgcaaa ttcaatgac atgacacacc ctccatgctt 240
 1063 gcattctcct gctcaactga cctcactctg agcacaacta agtgagctga ttttttggtg 300
 1064 ttcagacatt cagagattgc tggaagtgtt gcacttcctt catttgaggga gcacaagact 360
 1065 tcagttgtcg aaatggctac aactaattgc aagtatataa acaaggaggt gtgatgtgac 420
 1066 aggaaagatc ctgatgaagt gcttccttta tggaatgcct atctgaagtt tggactaaga 480
 1067 gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540
 1068 atgtttttat ttagatttag gatattgtgt ttctgccacc ggttcgactt ctcatattag 600
 1069 aaggcaagca gttagttcat atcttactac tttgcactat ttagatgga tgggtgaggga 660
 1070 ttgagaggct actactatta atgtgcgtaa actttgcac tttagctctc taaatgaaac 720
 1071 cggatgatgt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780
 -> 1072 aaaaaaaa
 1125 <210> SEQ ID NO: 23
 1126 <211> LENGTH: 603 1132 (p.2)
 1127 <212> TYPE: DNA
 1128 <213> ORGANISM: Zea mays
 1130 <220> FEATURE:
 1131 <221> NAME/KEY: unsure
 1132 <222> LOCATION: (441)
 1134 <220> FEATURE:
 1135 <221> NAME/KEY: unsure
 1136 <222> LOCATION: (447)

789 ← insert

RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/665,308A

TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

1138 <220> FEATURE:
 1139 <221> NAME/KEY: unsure
 1140 <222> LOCATION: (485)
 1142 <220> FEATURE:
 1143 <221> NAME/KEY: unsure
 1144 <222> LOCATION: (498)
 1146 <220> FEATURE:
 1147 <221> NAME/KEY: unsure
 1148 <222> LOCATION: (528)
 1150 <220> FEATURE:
 1151 <221> NAME/KEY: unsure
 1152 <222> LOCATION: (553)
 1154 <220> FEATURE:
 1155 <221> NAME/KEY: unsure
 1156 <222> LOCATION: (560)
 1158 <220> FEATURE:
 1159 <221> NAME/KEY: unsure
 1160 <222> LOCATION: (576)..(577)
 1162 <220> FEATURE:
 1163 <221> NAME/KEY: unsure
 1164 <222> LOCATION: (598)
 1166 <400> SEQUENCE: 23
 1167 aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggttaggct 60
 1168 tctccgcgct caccgcgcgc ctgcgcgcgc cctacctga ccgctgcttc ctccccgggg 120
 1169 gcgcgctccg gctcggcgac cagccctgga tggcgcgcct agccgcgcgc acctgcttcg 180
 1170 cgctcgcgcg caaggtcgag gagacgcgcg tgccgcgcgc cctcgacctc cagctctacg 240
 1171 ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc 300
 1172 tgctcgtgct ctccgcgctt ggggtggcgga tgcacctgt cagcccttc tcctacctcc 360
 1173 agcccgctct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgc ctgctcgcgg 420
 1174 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggcccgc gccgcgttgc 480
 1175 tgatcacagc cgccgcgcgc gacggcggcg acggcgacgc cgacacggag ctcttggcgc 540
 1176 tcatcaatgc ccccgaggac aagaccgcgc agtgtgccaa gatcatctcc gaggtgacgc 600
 1177 gcatgagctt cctcgcctgc gatgtcggcg tgagcgccgc aaataagcgt aagcacgcgc 660
 1178 cggcgcagtt gtactgcgcg ccgcgcgagc cgagcggcgc gatcggcgc ctgtcctgct 720
 1179 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtggggcg 780
 1180 cgtcggcgtc cgtgtccgtg tcgtcctctc cagagccacc aggtcgggccc cccaagcgcg 840
 1181 cagcggcggc gtcggcgctc gcgtcggcgt cagccggggc cgccgccacc gtccaggtcc 900
 1182 cgcacagct acccccgac gaggagagcc gcgacgcctg gcgctccacc tgcgcgcgc 960
 1183 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcgggtggc ggtggagaat 1020
 1184 ggagaacaag gagcatcatt ggctcgcgct ggtgagcagg agaacgaact attttgccca 1080
 -> 1185 ttgccgtgac agatgggggg tgttcaactgc gtggagccgc gctgancaat ga 1132
 1606 <210> SEQ ID NO: 32
 1607 <211> LENGTH: 373
 1608 <212> TYPE: PRT
 1609 <213> ORGANISM: Nicotiana tabacum
 1611 <400> SEQUENCE: 32
 1612 Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu
 1613 1 5 10 15
 1615 Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Glu Lys Trp Gly Asp Leu

see item 9 on Euro Summary Sheet
P.3

RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/665,308A

TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

```

1616          20          25          30
1618 Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr
1619          35          40          45
1621 Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu
1622          50          55          60
1624 Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe
1625 65          70          75          80
1627 Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp
1628          85          90          95
1630 Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys
1631          100         105         110
1633 Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile
1634          115         120         125
1636 Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys
1637          130         135         140
1639 Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala
1640 145          150          155          160
1642 Lys Val Glu Glu Thr Gln Val Pro Leu Leu Leu Asp Phe Gln Val Glu
1643          165         170         175
1645 Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu
1646          180         185         190
1648 Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu
1649          195         200         205
1651 Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile
1652          210         215         220
1654 His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met
1655 225         230         235         240
1657 Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala
1658          245         250         255
1660 Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp
1661          260         265         270
1663 Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val
1664          275         280         285
1666 Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser
1667          290         295         300
1669 His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile
1670 305         310         315         320
1672 Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu
1673          325         330         335
1675 Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu
1676          340         345         350
1678 Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala
1679          355         360         365
1681 Val Gly Ser Pro His
1682          370

```

-> 1685 6
Delete

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/665,308A

DATE: 07/31/2001

TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:156 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:157 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:159 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:161 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:162 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:163 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:204 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:207 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:213 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:291 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:293 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:294 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:295 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:388 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:442 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:466 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:761 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:762 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:786 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

VERIFICATION SUMMARY

DATE: 07/31/2001

PATENT APPLICATION: US/09/665,308A

TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

L:807 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:809 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1005 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1006 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1008 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1010 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1011 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1038 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1050 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1072 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:789 SEQ:21
L:1095 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1116 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1185 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1185 M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:1132 SEQ:23
L:1283 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1284 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1330 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1333 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1336 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1685 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32